

334 GGCACCGAGCCAAATGGAGAGGTTGGAGCTGGAGTAGCGTGTGATGATTACTT 393
 Db 117 SetPrp-----SerglylysSerMetGlyGlyAsnLyhsCysAlaGluMetSerSer 134
 Qy 394 GCATGGAGGAAATCCCTCACCATCTCAAGCCCCGCACTGTGGAGCCCTGGAGA 453
 Db 135 AsparAsnPhelThrTrpSerSerAsnGluGlyAsnLyhsCysAlaGluMetSerSer 134
 Qy 454 AGCACAGCATTCTGGAGTGGAAAGTATAACTGTAACTGTGAGGTAACTCTATGCTGC 513
 Qy 155 Lys 155
 Db 514 AAA 516

RESULT 10
 US-08-422-166-4
 Sequence 4, Application US/88422166
 General Information:
 APPLICANT: IOVANNA, JUAN-LUCIO
 APPLICANT: KEM, VOLKER
 APPLICANT: DRAGORN, JEAN-CHARLES
 TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
 TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/422,166
 FILING DATE: 14-APR-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/778,156
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 595086man P.
 REFERENCE NUMBER: 24,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-4500
 TELEFAX: (703) 486-2347
 TELEX: 24855 OPAT UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 522 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: pancreas

ed. No.: 5,02e-18 Length: 522
 ore: 218,00 Match: 53
 recent Similarity: 50,31% Conservative: 28

RESULT 10
 US-09-525-041-2 (1-158) x US-08-422-166-4 (1-522)
 Sequence 10
 General Information:
 APPLICANT: IOVANNA, JUAN-LUCIO
 APPLICANT: KEM, VOLKER
 APPLICANT: DRAGORN, JEAN-CHARLES
 TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
 TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: P.C.
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/422,166
 FILING DATE: 14-APR-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/778,156
 FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 595086man P.
 REFERENCE NUMBER: 24,618
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-4500
 TELEFAX: (703) 486-2347
 TELEX: 24855 OPAT UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 522 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: pancreas

ed. No.: 5,02e-18 Length: 522
 ore: 218,00 Match: 53
 recent Similarity: 50,31% Conservative: 28

RESULT 11
 US-07-778-156-12
 Sequence 12, Application US/07778156
 General Information:
 APPLICANT: IOVANNA, JUAN-LUCIO
 APPLICANT: KEM, VOLKER
 APPLICANT: DRAGORN, JEAN-CHARLES
 TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
 TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/778,156
 FILING DATE: 1991219
 CLASSIFICATION: 435

ed. No.: 5,02e-18 Length: 522
 ore: 218,00 Match: 53
 recent Similarity: 50,31% Conservative: 28

L3 ANSWER 58 OF 59 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 1993:432762 BIOSIS
DN PREV199396087387
TI A gene homologous to the **reg** gene is
expressed in the human pancreas.
AU Bartoli, Catherine; Gharib, Bouchra; Giorgi, Dominique; Sansonetti, Alice;
Dagorn, Jean-Charles; Berge-Lefranc, Jean-Louis [Reprint author]
CS Unite 315 l'INSERM, 46 Boulevard Gaye, 13258 Marseille Cedex 9, France
SO FEBS (Federation of European Biochemical Societies) Letters, (1993) Vol.
327, No. 3, pp. 289-293.
CODEN: FEBLAL. ISSN: 0014-5793.
DT Article
LA English
OS Genbank-L08010
ED Entered STN: 22 Sep 1993
Last Updated on STN: 6 Nov 1993
AB We have determined the nucleotide sequence of reg1 a **human**
genomic DNA fragment homologous to the **reg** gene which is
expressed in the exocrine pancreas and regenerating islets.
Sequence comparisons of **reg** and reg1 suggested similar
exon-intron organisation. Based on this assumption, specific
oligonucleotides for reg1 exons were used to demonstrate expression of the
reg1 gene in pancreas and liver. The proteins encoded by **reg** and
reg1 comprise 166 amino acids and differ by 22 amino acids only.

Db 92 STDSDSNWIGLUDPKKQRWHRHSSGSLVSYKWDGTGSPSSANAGYCYASLTSCLGPKKKWD 151
 Qy 144 NECNKROHFLCKYR 157
 Db 152 ESECKKESFVCKR 165

RESULT 7
 LIT2_MOUSE STANDARD; PRT; 173 AA.
 ID LIT2_MOUSE STANDARD; PRT; 173 AA.
 AC 008731;
 DT 01-NOV-1995 (Rel. 32. Created)
 DT 28-FEB-2003 (Rel. 41. Last annotation update)
 DE Lithostathine 2 precursor (Pancreatic thread protein 2) (PPTP) (islet of langerhans regenerating protein 2) (REG 2).
 DE PROTEIN REG2.
 OS Mus musculus (Mouse).
 RX MEDLINE=93340209; PubMed=8340418;
 RA Unno M., Yonekura H., Nakagawa K.-I., Watanabe T., Miyashita H.,
 RA Morizumi S., Okamoto H., Itoh T., Terada H.;
 OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 RA Unno M., Yonekura H., Nakagawa K.-I., Watanabe T., Miyashita H.,
 RA Morizumi S., Okamoto H., Itoh T., Terada H.;
 OC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RT "STRUCTURE, chromosomal localization, and expression of "mouse reg genes, reg I and reg II. A novel type of reg gene, reg II, exists in the mouse genome.";
 J. Biol. Chem. 268:15974-15982(1993).
 CC -- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM CARBONATE PRECIPITATION.
 CC -- TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS AND NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS.
 CC EXPRESSED STRONGER IN PANCREAS, WEAKLY IN LIVER, BUT NOT AT ALL.
 CC IN GALLBLADDER.
 CC -- SIMILARITY: Contains 1 C-type lectin family domain.

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CC EMBL; D14011; BAA0112.1; -.
 DR B47148; BAA0112.1.
 DR P04511; LIT2.
 DR MGD; MGI:97896; REG2.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR00390; Pancreaticis_ac.
 DR PFam; PF00059; Lectin_C; 1.
 DR PRINTS; PRO1504; PNCHEATITSAP.
 DR PRINTS; PRO0556; ANTFREEZEII.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 DR KW Signal; Lectin.
 PT SIGNAL; 1; 22 BY SIMILARITY.
 PT CHAIN; 23; 173 LITHOSTATHINE 2.
 PT DOMAIN; 41; 171 C-TYPE LECTIN (LONG FORM).
 PT DISULFID; 43; 54 BY SIMILARITY.
 PT DISULFID; 71; 169 BY SIMILARITY.
 PT DISULFID; 144; 161 BY SIMILARITY.
 PT SEQUENCE; 173 AA; 19407 MW; 7D34C4DAB23225C CRC64;

Query Match Score 26.9%; Score 236.5%; Score 233; DB 1; Length 135; Best Local Similarity 34.4%; Pred. No. 1.7e-16; Matches 45; Conservative 18; Mismatches 64; Indels 4; Gaps 2; SQ SEQUENCE 135 AA; 16291 MW; 04BAC45D52B721C8 CRC64;

Matches 50; Conservative 33; Mismatches 72; Indels 19; Gaps 5;
 Qy 1 MASRSMRLILLLSCLAKTGVLGPI-----MRPSCAPGWFYHNSNCYGYFRK 47
 Db 1 MAQNVVLLIFLCLMFLSISQGQVAEDFFPLAKSAINCPEGANAYGSYCYLBD 60

RESULT 8
 LECG_CROT STANDARD; PRT; 135 AA.
 ID LECG_CROT STANDARD; PRT; 135 AA.
 AC P21963;
 DT 01-AUG-1991 (Rel. 19. Created)
 DT 01-AUG-1991 (Rel. 19. Last annotation update)
 DT 15-SEP-2003 (Rel. 42. Last annotation update)
 DR Galactose-specific lectin.
 OS Crotalus atrox (Western diamondback rattlesnake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Crotalus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=venom;
 RX MEDLINE=9115849; PubMed=1989986;
 RA Hirabayashi J., Kusunoki T., Kasai K.-I.;
 RT "Complete primary structure of a galactose-specific lectin from the venom of the rattlesnake Crotalus atrox. Homologies with Ca2(+)-dependent-type lectins.";
 RT J. Biol. Chem. 266:23220-23226(1991).
 CC -- FUNCTION: Galactose-binding protein which recognizes specific carbohydrate structures and agglutinates a variety of animal cells by binding to cell-surface glycoproteins and glycolipids. Calcium-dependent lectin. Shows high hemagglutinating activity.
 CC -- SUBUNIT: Homodimer; disulfide-linked.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- SIMILARITY: Contains 1 C-type lectin family domain.
 DR PIR; A38609; A38609.
 DR HSSP; P22897; LECG.
 DR InterPro; IPR002353; AntifreezeII.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR00390; Pancreaticis_ac.
 DR PFam; PF00059; Lectin_C; 1.
 DR PRINTS; PRO1504; PNCHEATITSAP.
 DR PRINTS; PRO0556; ANTFREEZEII.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS500615; C_TYPE_LECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 DR KW Calcium; Lectin.
 PT DOMAIN; 1; 135 C-TYPE LECTIN (LONG FORM).
 PT DISULFID; 3; 14
 PT DISULFID; 31; 131
 PT DISULFID; 38; 133
 PT DISULFID; 106; 123
 PT DISULFID; 86; 86 INTERCHAIN.
 PT SEQUENCE 135 AA; 16291 MW; 04BAC45D52B721C8 CRC64;

Query Match Score 26.5%; Score 233; DB 1; Length 135; Best Local Similarity 34.4%; Pred. No. 1.7e-16; Matches 45; Conservative 18; Mismatches 64; Indels 4; Gaps 2; SQ SEQUENCE 135 AA; 16291 MW; 04BAC45D52B721C8 CRC64;

Qy 29 SCAPGWFYHNSNCYGYFRKANWDALETCOSYKWDGTGSPSSANAGYCYASLTSCLGPKKKWD 151
 Db 2 NCPLDMLPMGLCYKIFNQLCWDEAMFCKYKPGCHLASPHRYGSESLIAEVISDYK 61

Query Match Score 26.9%; Score 236.5%; DB 1; Length 173; Best Local Similarity 28.7%; Pred. No. 9.8e-17; Matches 50; Conservative 33; Mismatches 72; Indels 19; Gaps 5;